WHAT IS CLAIMED IS:

1. A method for detecting a nucleic acid-binding protein comprising the steps of:

(a) contacting a nucleic acid molecule comprising a nucleic acid-binding sequence with a protein sample potentially containing an unknown nucleic acid-binding protein under conditions sufficient to form a binding complex, wherein the binding complex protects bound nucleic acid from degradation;

(b) subjecting the binding complex to nucleic acid degradation conditions which degrade any unbound nucleic acid molecules; and

(c) detecting any bound nucleic acid, wherein detecting said bound nucleic acid indicates a nucleic acid-binding protein.

2. The method according to claim 1, further comprising the step of characterizing the nucleic acid-binding protein.

3. The method according to claim 2, wherein step of characterizing the nucleic acid-binding protein comprises a technique selected from the group consisting of immunodetection, mass spectrometry, amino acid sequencing, and enzymatic digestion of the DNA-binding protein.

4. The method according to claim 3, wherein the immunodetection comprises the steps of:

(a) contacting antibodies raised against known nucleic acid-binding proteins with the nucleic acid-binding protein under conditions sufficient to form a protein-antibody complex;

(b) detecting the protein-antibody complex; and

(c) characterizing the nucleic acid-binding protein of the protein-antibody complex.

5. The method according to claim 4, wherein the protein-antibody complex further comprises the bound nucleic acid molecule.

6. The method according to claim 1, wherein the protein sample of step (a) is selected from the group consisting of a cell extract, a purified protein, and a partially purified protein.

7. The method according to claim 6, wherein the cell extract is prepared from prokaryotic cells.

8. The method according to claim 6, wherein the cell extract is prepared from eukaryotic cells.

9. The method according to claim 8, wherein the eukaryotic cell is a mammalian cell.

10. The method according to claim 9, wherein the mammalian cell is a human cell.

11. The method according to claim 1, wherein the nucleic acid molecule is DNA.

12. The method according to claim 1, wherein the nucleic acid molecule is RNA.

13. The method according to claim 1, wherein the nucleic acid molecule of step (a) is selected from the group consisting of a mRNA, a synthetic RNA, cDNA, a PCR product, a DNA restriction fragment, a recombinant molecule, a genomic or partial genomic library, a cDNA library, a cDNA library, a synthetic DNA and combinations thereof.

14. The method according to claim 1, wherein the nucleic acid molecule contains a label.

15. The method according to claim 1, wherein step (c) comprises the step of detecting the label of the bound nucleic acid.

16. The method according to claim 5, wherein step of detecting the label comprises the step of using a detection system selected from the group consisting of a fluorescence detection system, a radioactive detection system, an enzyme-linked detection system, and a biotinylation detection system.

17. The method according to claim 4, wherein the label is a radioisotope.

18. The method according to claim 4, wherein the label is biotin.

19. The method according to claim 4, wherein the label is a fluorophore.

20. The method according to claim 7, wherein the radioisotope is selected from the group consisting of 32P, 33P, or 35S.

21. The method according to claim 9, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative, Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

22. The method of claim 8, wherein the step of detecting the label further comprises contacting the biotin with a binding partner.

23. The method of claim 2, wherein the binding partner is selected from the group of avidin, streptavidin, and anti-biotin antibody.

24. The method of claim 2, wherein the binding partner is conjugated to a fluorophore.

25. The method according to claim 4, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative, Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

26. The method according to claim 1, wherein step (c) comprises the steps of:

(c_i) contacting the bound nucleic acid with a nucleic acid dye;

(c_{ii}) detecting the nucleic acid dye.

27. The method according to claim 26, wherein the nucleic acid dye is selected from the group consisting of cyanine, cyanine-derivatives, PicoGreen, OliGreen, RiboGreen, TOTO dyes, intercalating dyes, ethidium bromide, propridium iodide, hexidium idodide, acridine orange, minor-groove-binding dyes, Hoeschst, and DAPI.

28. The method according to claim 1, wherein the nucleic acid degradation conditions are enzymatic.

29. The method according to claim 1, wherein the nucleic acid degradation conditions are enzymatic and physical.

30. The method according to claim 29, wherein the physical conditions comprise heat and alkali.

31. The method according to claim 1, wherein the nucleic acid molecule of step (a) further comprises a chemical modification enabling degradation of the nucleic acid molecule by an enzyme.

32. The method according to claim 31, wherein the chemical modification is introduced in the nucleotide base of one or more guanine, cytosine, thymine, or adenosine.

33. The method according to claim 32, wherein the enzyme that degrades the unbound nucleic acid molecule is a DNA N-glycosylase.

34. The method according to claim 32, wherein the enzyme that degrades the unbound nucleic acid molecule is selected from the group consisting of a DNA N-glycosylase, AP lyase, and combinations thereof.

35. The method according to claim 33, wherein the DNA N-glycosylase is selected from the group consisting of uracil DNA glycosylase, 3-methyladenine DNA glycosylase I, 3-methyladenine DNA glycosylase II, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, thymine mismatch DNA glycosylase, and 8-oxoguanosine DNA glycosylase.

36. The method according to claim 34, wherein the AP lyase is selected from the group consisting of, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, exonuclease III and endonuclease IV.

37. The method according to claim 33, wherein degradation of the nucleic acid molecule comprises the steps of:

(b_i) contacting the nucleic acid molecule with the DNA *N*-glycosylase;

(b_{ii}) excising one or more nucleotide bases of the DNA molecule having the chemical modification;

(b_{iii}) forming an AP site at each excised nucleotide base; and

(b_{iv}) exposing the nucleic acid molecule to heat and alkali conditions to cause break in the nucleic acid molecule at each AP site.

38. The method according to claim 34, wherein degradation of the nucleic acid molecule comprises the steps of:

(b_i) contacting the nucleic acid molecule with the DNA *N*-glycosylase;

(b_{ii}) excising one or more nucleotide bases of the nucleic acid molecule having the chemical modification;

(b_{iii}) forming an AP site at each excised nucleotide base;

(b_{iv}) contacting the nucleic acid molecule with the AP lyase;

(b_{v}) forming a single-base lesion at each AP site; and

(b_{vi}) exposing the nucleic acid molecule to heat and alkali conditions to cause a break in the nucleic acid molecule at each single-base lesion.

39. The method according to claim 1, wherein step (b) comprises the step of contacting the binding complex with an enzyme in an amount sufficient to degrade unbound nucleic acid molecules.

40. The method according to claim 39, wherein the enzyme is a DNase.

41. The method according to claim 39, wherein the enzyme is an RNase.

42. The method according to claim 1, wherein the binding complex comprises a sequence-specific interaction between the nucleic acid-binding protein and the nucleic acid-binding sequence.

43. The method according to claim 1, wherein the binding complex comprises a non-sequence-specific interaction between the nucleic acid-binding protein and the nucleic acid-binding sequence.

44. A method for detecting a DNA-binding protein comprising the steps of:

(a) combining at least one DNA molecule, comprising a DNA-binding sequence and a label, with at least one protein sample potentially containing at least one unknown DNA-binding protein, in a reaction vessel comprising a plurality of wells;

(b) exposing the DNA molecule and the protein sample in the reaction vessel to conditions sufficient to form a binding complex, comprising the DNA-binding protein and a bound DNA molecule, wherein the binding complex protects the bound DNA molecule or fragment thereof from degradation;

(c) subjecting the binding complex to DNA degradation conditions, wherein any unbound DNA molecules are degraded; and

(d) detecting any bound DNA, wherein detecting said bound DNA indicates a DNA-binding protein,

wherein said method is high-throughput.

45. The method according to claim 44, further comprising the step of characterizing the DNA-binding protein.

46. The method according to claim 45, wherein the step of characterizing the DNA-binding protein comprises a technique selected from the group consisting of immunodetection, mass spectrometry, amino acid sequencing, and enzymatic digestion of the DNA-binding protein.

47. The method according to claim 46, wherein the immunodetection comprises the steps of:

(a) contacting antibodies raised against known DNA-binding proteins with the DNA-binding protein under conditions sufficient to form a protein-antibody complex;

(b) detecting the protein-antibody complex; and

(c) characterizing the DNA-binding protein of the protein-antibody complex.

48. The method according to claim 47, wherein the protein-antibody complex further comprises the bound DNA molecule.

49. The method according to claim 44, wherein the method is automated.

50. The method according to claim 44, wherein step (a) further comprises binding said at least one DNA molecule to a magnetic microparticle in said reaction vessel.

51. The method according to claim 44, wherein the protein sample of step (a) is selected from the group consisting of a cell extract, a purified protein, and a partially purified protein.

52. The method according to claim 51, wherein the cell extract is prepared from prokaryotic cells.

53. The method according to claim 52, wherein the cell extract is prepared from eukaryotic cells.

54. The method according to claim 53, wherein the eukaryotic cell is a mammalian cell.

55. The method according to claim 54, wherein the mammalian cell is a human cell.

56. The method according to claim 44, wherein the DNA molecule of step (a) is selected from the group consisting of a cDNA, a PCR product, a DNA restriction fragment, a recombinant molecule, a genomic or partial genomic library, a cDNA library, a synthetic DNA and combinations thereof.

57. The method according to claim 44, wherein the DNA molecule contains a label.

58. The method according to claim 44, wherein step (d) comprises the step of detecting the label the bound DNA.

59. The method according to claim 58, wherein step of detecting the label comprises the step of using a detection system selected from the group consisting of a fluorescence detection system, a radioactive detection system, an enzyme-linked detection system, and a biotinylation detection system.

60. The method according to claim 58, wherein the label is a radioisotope.

61. The method according to claim 58, wherein the label is biotin.

62. The method according to claim 58, wherein the label is a fluorophore.

63. The method according to claim 60, wherein the radioisotope is selected from the group consisting of 32P, 33P, or 35S.

64. The method according to claim 62, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative, Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

65. The method of claim 61, wherein the step of detecting the label further comprises contacting the biotin with a binding partner.

66. The method according to claim 65, wherein the binding partner is selected from the group of avidin, streptavidin, and anti-biotin antibody.

67. The method according to claim 65, wherein the binding partner is conjugated to a fluorophore.

68. The method according to claim 67, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative, Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

69. The method according to claim 44, wherein step (e) comprises the steps of:

(d_i) contacting the bound DNA with a nucleic acid dye;

(d_{ii}) detecting the nucleic acid dye.

70. The method according to claim 69, wherein the nucleic acid dye is selected from the group consisting of cyanine, cyanine-derivatives, PicoGreen, OliGreen, RiboGreen, TOTO dyes, intercalating dyes, ethidium bromide, propridium iodide, hexidium idodide, acridine orange, minor-groove-binding dyes, Hoeschst, and DAPI.

71. The method according to claim 44, wherein the DNA degradation conditions are enzymatic.

72. The method according to claim 44, wherein the DNA degradation conditions are enzymatic and physical.

73. The method according to claim 72, wherein the physical conditions comprise heat and alkali.

74. The method according to claim 44, wherein the DNA molecule of step (a) further comprises a chemical modification enabling degradation of the DNA molecule by an enzyme.

75. The method according to claim 74, wherein the chemical modification is introduced in the nucleotide base of one or more guanine, cytosine, thymine, or adenosine.

76. The method according to claim 74, wherein the enzyme that degrades the unbound DNA molecule is a DNA N-glycosylase.

77. The method according to claim 74, wherein the enzyme that degrades the unbound DNA molecule is selected from the group consisting of a DNA N-glycosylase and an AP lyase.

78. The method according to claim 76, wherein the DNA N-glycosylase is selected from the group consisting of uracil DNA glycosylase, 3-methyladenine DNA glycosylase I, 3-methyladenine DNA glycosylase II, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, thymine mismatch DNA glycosylase, and 8-oxoguanosine DNA glycosylase.

79. The method according to claim 77, wherein the AP lyase is selected from the group consisting of, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, exonuclease III and endonuclease IV.

80. The method according to claim 76, wherein degradation of the DNA molecule comprises the steps of:

(c_i) contacting the DNA molecule with the DNA *N*-glycosylase;

(c_{ii}) excising one or more nucleotide bases of the DNA molecule having the chemical modification;

(c_{iii}) forming an AP site at each excised nucleotide base; and

(c_{iv}) exposing the DNA molecule to heat and alkali conditions to cause a break in the DNA molecule at each AP site.

81. The method according to claim 161, wherein degradation of the DNA molecule comprises the steps of:

(c_i) contacting the DNA molecule with the DNA *N*-glycosylase;

(c_{ii}) excising one or more nucleotide bases of the DNA molecule having the chemical modification;

(c_{iii}) forming an AP site at each excised nucleotide base;

(c_{iv}) contacting the DNA molecule with the AP lyase;

(c_{v}) forming a single-base lesion at each AP site; and

(c_{vi}) exposing the DNA molecule to heat and alkali conditions to cause a break in the DNA molecule at each single-base lesion.

82. The method according to claim 44, wherein step (c) comprises the step of contacting the binding complex with an enzyme in an amount sufficient to degrade unbound DNA molecules.

83. The method according to claim 82, wherein the enzyme is a DNase.

84. The method according to claim 44, wherein the binding complex comprises a sequence-specific interaction between the DNA-binding protein and the DNA-binding sequence.

85. The method according to claim 44, wherein the binding complex comprises a non-sequence-specific interaction between the DNA-binding protein and the DNA-binding sequence.

86. A method for detecting an inhibitor of a nucleic acid-binding protein comprising the steps of:

(a) preparing a first reaction mixture by combining at least one protein sample potentially containing one or more unknown nucleic acid-binding proteins with a nucleic acid molecule, comprising a label and nucleic acid-binding sequence, in a first well of a reaction vessel under conditions sufficient to

form a binding complex, comprising the nucleic acid-binding protein and the nucleic acid-binding sequence;

(b) preparing a second reaction mixture by combining the protein sample of the first reaction with a nucleic acid molecule of the first reaction and at least one chemical sample potentially containing one or more inhibitors of the nucleic acid-binding protein in a second well of a reaction vessel under conditions sufficient to form the binding complex, wherein the inhibitor prevents the formation of the binding complex;

(c) treating the first and second reaction mixtures in a manner sufficient to degrade unbound nucleic acid molecules; and

(d) detecting the amount of intact nucleic acid of both first and second reaction mixtures, wherein less amount of intact nucleic acid of said second reaction mixture indicates the presence of an inhibitor.

87. The method according to claim 86, further comprising the step of isolating the inhibitor.

88. The method according to claim 86, wherein the protein sample of step (a) is selected from the group consisting of a cell extract, a purified protein, and a partially purified protein.

89. The method according to claim 88, wherein the cell extract is prepared from prokaryotic cells.

90. The method according to claim 88, wherein the cell extract is prepared from eukaryotic cells.

91. The method according to claim 90, wherein the eukaryotic cell is a mammalian cell.

92. The method according to claim 91, wherein the mammalian cell is a human cell.

93. The method according to claim 86, wherein the nucleic acid molecule of step (a) is selected from the group consisting of a mRNA, cDNA, a PCR product, a DNA restriction fragment, a recombinant molecule, a genomic or partial genomic library, a cDNA library, a synthetic DNA, a synthetic RNA and combinations thereof.

94. The method according to claim 86, wherein the nucleic acid molecule contains a label.

95. The method according to claim 86, wherein step (d) comprises the step of detecting the label of the intact nucleic acid.

96. The method according to claim 95, wherein step of detecting the label comprises the step of using a detection system selected from the group consisting of a fluorescence detection system, a radioactive detection system, an enzyme-linked detection system, and a biotinylation detection system.

97. The method according to claim 95, wherein the label is a radioisotope.

98. The method according to claim 95, wherein the label is biotin.

99. The method according to claim 95, wherein the label is a fluorophore.

100. The method according to claim 97, wherein the radioisotope is selected from the group consisting of 32P, 33P, or 35S.

101. The method according to claim 99, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative,

Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

102. The method according to claim 98, wherein the step of detecting the label further comprises contacting the biotin with a binding partner.

103. The method according to claim 102, wherein the binding partner is selected from the group of avidin, streptavidin, and anti-biotin antibody.

104. The method according to claim 103, wherein the binding partner is conjugated to a fluorophore.

105. The method according to claim 104, wherein the fluorophore is selected from the group consisting of fluorescein, fluorescein-derivative, rhodamine, rhodamine-derivative, Texas Red, Oregon Green, Alexa Fluor, Cascade Blue, Tetramethylrhodamine, Pacific Blue, SYBR, and BODIPY.

106. The method according to claim 86, wherein step (d) comprises the steps of:

(d_i) contacting the intact nucleic acid with a nucleic acid dye;

(d_{ii}) detecting the nucleic acid dye.

107. The method according to claim 106, wherein the nucleic acid dye is selected from the group consisting of cyanine, cyanine-derivatives, PicoGreen, OliGreen, RiboGreen, TOTO dyes, intercalating dyes, ethidium bromide, propridium iodide, hexidium idodide, acridine orange, minor-groove-binding dyes, Hoeschst, and DAPI.

108. The method according to claim 86, wherein the nucleic acid degradation conditions are enzymatic.

109. The method according to claim 86, wherein the nucleic acid degradation conditions are enzymatic and physical.

110. The method according to claim 109, wherein the physical conditions comprise heat and alkali.

111. The method according to claim 86, wherein the nucleic acid molecule of step (a) further comprises a chemical modification enabling degradation of the nucleic acid molecule by an enzyme.

112. The method according to claim 111, wherein the chemical modification is introduced in the nucleotide base of one or more guanine, cytosine, thymine, or adenosine.

113. The method according to claim 111, wherein the enzyme that degrades the unbound nucleic acid molecule is a DNA N-glycosylase.

114. The method according to claim 111, wherein the enzyme that degrades the unbound nucleic acid molecule is selected from the group consisting of an DNA N-glycosylase, an AP lyase, and combinations thereof.

115. The method according to claim 113, wherein the DNA N-glycosylase is selected from the group consisting of uracil DNA glycosylase, 3-methyladenine DNA glycosylase I, 3-methyladenine DNA glycosylase II, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, and thymine mismatch DNA glycosylase.

116. The method according to claim 114, wherein the AP lyase is selected from the group consisting of, pyrimidine hydrate DNA glycosylase (endonuclease III), formamidopyrimidine (FaPy) DNA glycosylase, exonuclease III and endonuclease IV.

117. The method according to claim 113, wherein degradation of the nucleic acid molecule comprises the steps of:

(d_i) contacting the nucleic acid molecule with the DNA *N*-glycosylase;

(d_{ii}) excising one or more nucleotide bases of the nucleic acid molecule having the chemical modification;

(d_{iii}) forming an AP site at each excised nucleotide base; and

(d_{iv}) exposing the nucleic acid molecule to heat and alkali conditions to cause a break in the nucleic acid molecule at each AP site.

118. The method according to claim 114, wherein degradation of the nucleic acid molecule comprises the steps of:

(d_i) contacting the nucleic acid molecule with the DNA *N*-glycosylase;

(d_{ii}) excising one or more nucleotide bases of the nucleic acid molecule having the chemical modification;

(d_{iii}) forming an AP site at each excised nucleotide base;

(d_{iv}) contacting the nucleic acid molecule with the AP lyase;

(d_v) forming a single-base lesion at each AP site; and

(d_{vi}) exposing the nucleic acid molecule to heat and alkali conditions to cause a break in the nucleic acid molecule at each single-base lesion.

119. The method according to claim 86, wherein step (e) comprises the step of contacting the first and second reaction mixtures with an enzyme in an amount sufficient to degrade unbound nucleic acid molecules.

120. The method according to claim 119, wherein the enzyme is a DNase

121. The method according to claim 119, wherein the enzyme is a RNase.

122. The method according to claim 86, wherein the binding complex comprises a sequence-specific interaction between the nucleic acid-binding protein and the nucleic acid-binding sequence.

123. The method according to claim 86, wherein the binding complex comprises a non-sequence-specific interaction between the nucleic acid-binding protein and the nucleic acid-binding sequence.

124. The method according to claim 86, wherein the nucleic acid molecule is DNA or RNA.

125. The methods according to claims 1, 44, and 86 are automated

126. The methods according to claims 1, 44 and 86 are high-throughput

127. A kit for carrying out the method according to claim 1, comprising protein samples potentially containing an unknown nucleic acid-binding protein, a nucleic acid molecule comprising a nucleic acid-binding sequence, components for preparing the nucleic acid molecule, a label, an enzyme to attach the label to the nucleic acid molecule, an enzyme to degrade or facilitate the degradation of unbound nucleic acid, and reagents to assist in the degradation of unbound nucleic acid, and a detection system to detect the label of the nucleic acid128. The method according to claim 44, wherein the reaction vessel is a microtiter plate129. The method according to claim 44, wherein the reaction vessel comprises an array of wells ranging from 1 to 5,000.

130. The method according to claim 44, wherein the reaction vessel comprises an array of wells ranging from 1 to 1,000.

131. The method according to claim 44, wherein the reaction vessel comprises an array of wells ranging from 1 to 500.

132. The method according to claim 127, wherein the microtiter plate comprises 96 wells.

133. The method according to claim 127, wherein the microtiter plate comprises 384 wells.

134. The method according to claim 44, wherein the reaction vessel is a strip well unit.

135. The method according to claim 44, wherein the reaction vessel is a planar well unit.

136. The method according to claim 44, wherein the reaction vessel is a chip well unit.

137. The method according to claims 44, wherein the method further comprises step (e), wherein step (e) comprises validating the detection of the nucleic-acid binding protein.

138. The method according to claim 138, wherein step (e) further comprises the steps of:

(e_i) potential DNA-binding proteins contained in the one or more protein samples are detected according to steps (a) through (d) wherein the DNA and the protein samples are combined according to step (a) and exposed to conditions sufficient to form a binding complex according to step (b), wherein said conditions are low-stringency conditions sufficient to form non-specific binding complexes;

(e_{ii}) the protein samples containing a detected DNA-binding protein are contacted again with the DNA molecule and exposed to conditions that are of higher-stringency than step (e_i) that are sufficient to form a more highly-specific binding complex comprising the DNA-binding protein bound to its preferred

DNA-binding sequence, wherein the binding complex protects the bound DNA molecule or fragment thereof from degradation;

(e_{iii}) subjecting the binding complexes to DNA degradation conditions, wherein any unbound DNA molecules are degraded;

(e_{iv}) detecting any bound DNA, wherein detecting said bound DNA indicates the presence of a DNA-binding protein;

(e_{v}) repeating steps (e_{ii}) to (e_{iv}), wherein the stringency of the conditions of step (e_{ii}) are progressively increased each round.

139. A method for detecting a nucleic acid-binding protein comprising the steps of:

(a) contacting a nucleic acid molecule comprising a nucleic acid-binding sequence with a protein sample potentially containing an unknown nucleic acid-binding protein under conditions sufficient to form a binding complex, wherein the binding complex protects bound nucleic acid from degradation;

(b) subjecting the binding complex to nucleic acid degradation conditions which degrade any unbound nucleic acid molecules; and

(c) detecting any bound nucleic acid, wherein detecting said bound nucleic acid indicates a nucleic acid-binding protein;

wherein steps (a) through (c) are carried out in a well of a microtiter plate.

140. The method of claim 139, wherein the nucleic acid molecule is hybridized to a generic capture reagent.

141. The method of claim 140, wherein the generic capture reagent is poly(A)-IgG, wherein poly(A) is hybridized to the nucleic acid molecule and IgG is coupled to the well of the microtiter plate.

142. The method of claim 141, wherein the nucleic acid molecule of claim 140 is covalently coupled to FITC and the generic capture reagent of claim 141 is anti-FITC, wherein the anti-FITC is coupled to the well of the microtiter plate.

143. The method of claim 139, wherein the method is high-throughput.

144. The method of claim 139, wherein the method is automated.

145. A method of transmitting a result of an assay, said assay comprising the steps of:

(a) contacting a nucleic acid molecule comprising a nucleic acid-binding sequence with a protein sample potentially containing an unknown nucleic acid-binding protein under conditions sufficient to form a binding complex, wherein the binding complex protects bound nucleic acid from degradation;

(b) subjecting the binding complex to nucleic acid degradation conditions which degrade any unbound nucleic acid molecules; and

(c) detecting any bound nucleic acid, wherein detecting said bound nucleic acid indicates a nucleic acid-binding protein;

(d) characterizing the nucleic acid-binding protein wherein the characterized nucleic acid-binding protein constitutes the result of said assay.

146. The method of claim 145 wherein steps (a) through (c) are carried out in a microtiter plate.

147. The method according to claim 145, wherein step (d) further comprises a technique selected from the group consisting of immunodetection, mass spectrometry, amino acid sequencing, and enzymatic digestion of the DNA-binding protein.

148. A reaction vessel for carrying out the method of claim 1 wherein the reaction vessel is coated with IgG antibodies coupled to amino-poly(A) and the nucleic acid molecule of claim 1 comprises a T-tail.

149. A reaction vessel for carrying out the method of claim 1 wherein the reaction vessel is coated with anti-FITC antibodies and the nucleic acid molecule of claim 1 comprises FITC.

150. The reaction vessel of claims 148 and 149, wherein the reaction vessel is a microwell plate.

151. The kit for carrying out the method according to claim 1 comprising a DNA *N*-glycosylase, a DNA *N*-glycosylase reaction buffer, reagents to assist in the degradation of unbound nucleic acid, the reaction vessel of claim 148, and optional instructions.

152. The kit for carrying out the method according to claim 1 comprising a DNA *N*-glycosylase, a DNA *N*-glycosylase reaction buffer, reagents to assist in the degradation of unbound nucleic acid, the reaction vessel of claim 149, and optional instructions.